



Kuroda Revised Sequence Listing filed 2006-08-14
SEQUENCE LISTING

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Ohbayashi, Tetsuya

<120> Methods for Diagnosing Endometriosis-Related Diseases

<130> 2006_0025A

<140> 10/564,481

<141> 2006-01-13

<150> JP 2003-196455

<151> 2003-07-14

<160> 8

<170> PatentIn version 3.3

<210> 1

<211> 830

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (95)..(613)

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Met Ile Ile Tyr Arg Asp Leu
1 5

atc agc cac gat gag atg ttc tcc gac atc tac aag atc cgg gag atc 163
Ile Ser His Asp Glu Met Phe Ser Asp Ile Tyr Lys Ile Arg Glu Ile
10 15 20

gcg gac ggg ttg tgc ctg gag gtg gag ggg aag atg gtc agt agg aca 211
Ala Asp Gly Leu Cys Leu Glu Val Glu Gly Lys Met Val Ser Arg Thr
25 30 35

gaa ggt aac att gat gac tcg ctc att ggt gga aat gcc tcc gct gaa 259
Glu Gly Asn Ile Asp Asp Ser Leu Ile Gly Gly Asn Ala Ser Ala Glu
40 45 50 55

ggc ccc gag ggc gaa ggt acc gaa agc aca gta atc act ggt gtc gat 307
Gly Pro Glu Gly Glu Gly Thr Glu Ser Thr Val Ile Thr Gly Val Asp
60 65 70

att gtc atg aac cat cac ctg cag gaa aca agt ttc aca aaa gaa gcc 355
Ile Val Met Asn His His Leu Gln Glu Thr Ser Phe Thr Lys Glu Ala
75 80 85

tac aag aag tac atc aaa gat tac atg aaa tca atc aaa ggg aaa ctt 403
Tyr Lys Lys Tyr Ile Lys Asp Tyr Met Lys Ser Ile Lys Gly Lys Leu
90 95 100

gaa gaa cag aga cca gaa aga gta aaa cct ttt atg aca ggg gct gca 451
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Glu Glu Gln Arg Pro Glu Arg Val Lys Pro Phe Met Thr Gly Ala Ala
105 110 115

gaa caa atc aag cac atc ctt gct aat ttc aaa aac tac cag ttc ttt 499
Glu Gln Ile Lys His Ile Leu Ala Asn Phe Lys Asn Tyr Gln Phe Phe
120 125 130 135

att ggt gaa aac atg aat cca gat ggc atg gtt gct cta ttg gac tac 547
Ile Gly Glu Asn Met Asn Pro Asp Gly Met Val Ala Leu Leu Asp Tyr
140 145 150

cgt gag gat ggt gtg acc cca tat atg att ttc ttt aag gat ggt tta 595
Arg Glu Asp Gly Val Thr Pro Tyr Met Ile Phe Phe Lys Asp Gly Leu
155 160 165

gaa atg gaa aaa tgt taa caaatgtggc aattattttg gatctatcac 643
Glu Met Glu Lys Cys
170

ctgtcatcat aactggcttc tgcttgtcat ccacacaaca ccaggactta agacaaatgg 703

gactgatgtc atcttgagct cttcatttat tttgactgtg atttatttgg agtggaggca 763

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20 25 30

Gly Lys Met Val Ser Arg Thr Glu Gly Asn Ile Asp Asp Ser Leu Ile
35 40 45

Gly Gly Asn Ala Ser Ala Glu Gly Pro Glu Gly Glu Gly Thr Glu Ser
50 55 60

Thr Val Ile Thr Gly Val Asp Ile Val Met Asn His His Leu Gln Glu
65 70 75 80

Thr Ser Phe Thr Lys Glu Ala Tyr Lys Lys Tyr Ile Lys Asp Tyr Met
85 90 95

Lys Ser Ile Lys Gly Lys Leu Glu Glu Gln Arg Pro Glu Arg Val Lys
100 105 110

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Pro Phe Met Thr Gly Ala Ala Glu Gln Ile Lys His Ile Leu Ala Asn
115 120 125

Phe Lys Asn Tyr Gln Phe Phe Ile Gly Glu Asn Met Asn Pro Asp Gly
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